Validated By CRFValidator v 1.0.2

Application No: 10576807 Version No: 1.1

Input Set:

Output Set:

Started: 2007-08-13 15:15:47.946
Finished: 2007-08-13 15:15:48.651
Elapsed: 0 hr(s) 0 min(s) 0 sec(s) 705 ms
Total Warnings: 10
Total Errors: 0
No. of SeqIDs Defined: 12
Actual SeqID Count: 12

Error code		Error Description
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W	213	Artificial or Unknown found in <213> in SEQ ID (4)
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W	213	Artificial or Unknown found in <213> in SEQ ID (11)
W	213	Artificial or Unknown found in <213> in SEQ ID (12)

SEQUENCE LISTING

<110> Clark, Janet

<120> METHOD FOR IDENTIFYING COMPOUNDS THAT
AFFECT EXPRESSION OF TRYPTOPHAN HYDROXYLASE ISOFORM 2

<130> 21487YP

<140> 10/576,807
<141> 2006-04-21

<150> PCT/US2004/34619
<151> 2004-10-20

<150> 60/514,268
<151> 2003-10-24

<160> 12

<170> FastSEQ for Windows Version 4.0

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<211> 447
<212> PRT
<213> Mus musculus

<400> 1

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Gly Leu Ile Lys Val Leu Lys Ile Phe Gln Glu Asn His Val Ser Leu
        35                  40                  45
Leu His Ile Glu Ser Arg Lys Ser Lys Gln Arg Asn Ser Glu Phe Glu
    50                  55                  60
Ile Phe Val Asp Cys Asp Ile Ser Arg Glu Gln Leu Asn Asp Ile Phe
65                  70                  75                  80
Pro Leu Leu Lys Ser His Ala Thr Val Leu Ser Val Asp Ser Pro Asp
                85                  90                  95
Gln Leu Thr Ala Lys Glu Asp Val Met Glu Thr Val Pro Trp Phe Pro
            100                 105                 110
Lys Lys Ile Ser Asp Leu Asp Phe Cys Ala Asn Arg Val Leu Leu Tyr
        115                 120                 125
Gly Ser Glu Leu Asp Ala Asp His Pro Gly Phe Lys Asp Asn Val Tyr
    130                 135                 140
Arg Arg Arg Arg Lys Tyr Phe Ala Glu Leu Ala Met Asn Tyr Lys His
145                 150                 155                 160
Gly Asp Pro Ile Pro Lys Ile Glu Phe Thr Glu Glu Glu Ile Lys Thr
                165                 170                 175
Trp Gly Thr Ile Phe Arg Glu Leu Asn Lys Leu Tyr Pro Thr His Ala
            180                 185                 190
Cys Arg Glu Tyr Leu Arg Asn Leu Pro Leu Leu Ser Lys Tyr Cys Gly
        195                 200                 205
Tyr Arg Glu Asp Asn Ile Pro Gln Leu Glu Asp Val Ser Asn Phe Leu
    210                 215                 220
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Lys Glu Arg Thr Gly Phe Ser Ile Arg Pro Val Ala Gly Tyr Leu Ser
225                 230                 235                 240
Pro Arg Asp Phe Leu Ser Gly Leu Ala Phe Arg Val Phe His Cys Thr
                245                 250                 255
Gln Tyr Val Arg His Ser Ser Asp Pro Leu Tyr Thr Pro Glu Pro Asp
            260                 265                 270
Thr Cys His Glu Leu Leu Gly His Val Pro Leu Leu Ala Glu Pro Ser
        275                 280                 285
Phe Ala Gln Phe Ser Gln Glu Ile Gly Leu Ala Ser Leu Gly Ala Ser
    290                 295                 300
Glu Glu Thr Val Gln Lys Leu Ala Thr Cys Tyr Phe Phe Thr Val Glu
305                 310                 315                 320
Phe Gly Leu Cys Lys Gln Asp Gly Gln Leu Arg Val Phe Gly Ala Gly
                325                 330                 335
Leu Leu Ser Ser Ile Ser Glu Leu Lys His Ala Leu Ser Gly His Ala
            340                 345                 350
Lys Val Lys Pro Phe Asp Pro Lys Ile Ala Cys Lys Gln Glu Cys Leu
        355                 360                 365
Ile Thr Ser Phe Gln Asp Val Tyr Phe Val Ser Glu Ser Phe Glu Asp
    370                 375                 380
Ala Lys Glu Lys Met Arg Glu Phe Ala Lys Thr Val Lys Arg Pro Phe
385                 390                 395                 400
Gly Leu Lys Tyr Asn Pro Tyr Thr Gln Ser Val Gln Val Leu Arg Asp
                405                 410                 415
Thr Lys Ser Ile Thr Ser Ala Met Asn Glu Leu Arg Tyr Asp Leu Asp
            420                 425                 430
Val Ile Ser Asp Ala Leu Ala Arg Val Thr Arg Trp Pro Ser Val
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<210> 2
<211> 488
<212> PRT
<213> Mus musculus

<400> 2

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Ser Leu Thr Gln Asn Lys Ala Ile Lys Ser Glu Asp Lys Lys Ser Gly
        35                  40                  45
Lys Glu Pro Gly Lys Gly Asp Thr Thr Glu Ser Ser Lys Thr Ala Val
    50                  55                  60
Val Phe Ser Leu Lys Asn Glu Val Gly Gly Leu Val Lys Ala Leu Arg
65                  70                  75                  80
Leu Phe Gln Glu Lys His Val Asn Met Leu His Ile Glu Ser Arg Arg
                85                  90                  95
Ser Arg Arg Arg Ser Ser Glu Val Glu Ile Phe Val Asp Cys Glu Cys
            100                 105                 110
Gly Lys Thr Glu Phe Asn Glu Leu Ile Gln Leu Leu Lys Phe Gln Thr
        115                 120                 125
Thr Ile Val Thr Leu Asn Pro Pro Glu Ser Ile Trp Thr Glu Glu Glu
    130                 135                 140
Asp Leu Glu Asp Val Pro Trp Phe Pro Arg Lys Ile Ser Glu Leu Asp
145                 150                 155                 160
Arg Cys Ser His Arg Val Leu Met Tyr Gly Thr Glu Leu Asp Ala Asp
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                165                 170                 175
His Pro Gly Phe Lys Asp Asn Val Tyr Arg Gln Arg Arg Lys Tyr Phe
            180                 185                 190
Val Asp Val Ala Met Gly Tyr Lys Tyr Gly Gln Pro Ile Pro Arg Val
        195                 200                 205
Glu Tyr Thr Glu Glu Glu Thr Lys Thr Trp Gly Val Val Phe Arg Glu
    210                 215                 220
Leu Ser Lys Leu Tyr Pro Thr His Ala Cys Arg Glu Tyr Leu Lys Asn
225                 230                 235                 240
Leu Pro Leu Leu Thr Lys Tyr Cys Gly Tyr Arg Glu Asp Asn Val Pro
                245                 250                 255
Gln Leu Glu Asp Val Ser Met Phe Leu Lys Glu Arg Ser Gly Phe Thr
            260                 265                 270
Val Arg Pro Val Ala Gly Tyr Leu Ser Pro Arg Asp Phe Leu Ala Gly
        275                 280                 285
Leu Ala Tyr Arg Val Phe His Cys Thr Gln Tyr Val Arg His Gly Ser
    290                 295                 300
Asp Pro Leu Tyr Thr Pro Glu Pro Asp Thr Cys His Glu Leu Leu Gly
305                 310                 315                 320
His Val Pro Leu Leu Ala Asp Pro Lys Phe Ala Gln Phe Ser Gln Glu
                325                 330                 335
Ile Gly Leu Ala Ser Leu Gly Ala Ser Asp Glu Asp Val Gln Lys Leu
            340                 345                 350
Ala Thr Cys Tyr Phe Phe Thr Ile Glu Phe Gly Leu Cys Lys Gln Glu
        355                 360                 365
Gly Gln Leu Arg Ala Tyr Gly Ala Gly Leu Leu Ser Ser Ile Gly Glu
    370                 375                 380
Leu Lys His Ala Leu Ser Asp Lys Ala Cys Val Lys Ser Phe Asp Pro
385                 390                 395                 400
Lys Thr Thr Cys Leu Gln Glu Cys Leu Ile Thr Thr Phe Gln Asp Ala
                405                 410                 415
Tyr Phe Val Ser Asp Ser Phe Glu Glu Ala Lys Glu Lys Met Arg Asp
            420                 425                 430
Phe Ala Lys Ser Ile Thr Arg Pro Phe Ser Val Tyr Phe Asn Arg Tyr
        435                 440                 445
Thr Gln Ser Ile Glu Ile Leu Lys Asp Thr Arg Ser Ile Glu Asn Val
    450                 455                 460
Val Gln Asp Leu Arg Ser Asp Leu Asn Thr Val Cys Asp Ala Leu Asn
465                 470                 475                 480
Lys Met Asn Gln Tyr Leu Gly Ile
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<213> Artificial Sequence

<220>
<223> TPH2a riboprobe template

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ttggattctg ctgtgccaga agatcatcag ctacttggca gcttaacaca aaataaggct 120
atcaaaagcg aggacaagaa aagcggcaaa gagcccggca aaggcgacac cacagagagc 180
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<210> 4
<211> 219
<212> DNA
<213> Artificial Sequence

<220>
<223> TPH2b riboprobe

<400> 4
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cggtcccggc gaagaagttc tgaagtcgaa atcttcgtgg actgcgaatg tggcaaaacg 120
gaattcaatg agctcatcca gttgctgaaa tttcagacca ccattgtgac cctgaatccg 180
cctgagagca tttggacgga ggaagaagat ctcgaggat 219

<210> 5
<211> 818
<212> DNA
<213> Artificial Sequence

<220>
<223> TPH2c riboprobe

<400> 5
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aaaagcgagg acaagaaaag cggcaaagag cccggcaaag gcgacaccac agagagcagc 180
aagacagcag ttgtgttctc cttgaagaat gaagttggtg ggctggtgaa agcacttaga 240
ctattccagg aaaaacatgt caacatgctt catatcgaat ccaggcggtc ccggcgaaga 300
agttctaagt cgaaatcttc gtggactgcg aatgtggcaa aacggaattc aatgagctca 360
tccagttgct gaaatttcag accaccattg tgaccctgaa tccgcctgag agcatttgga 420
cggaggaaga agatctcgag gatgtgccgt ggttccctcg gaagatctct gagttagaca 480
gatgctctca ccgagtcctc atgtacggca ccgagcttga tgccgaccat ccaggattta 540
aggacaatgt ctatcgacag aggaggaagt attttgtgga tgtggccatg ggctataaat 600
atggtcagcc cattcccagg gtcgagtaca cagaagaaga gactaaaact tggggtgttg 660
tgttccggga gctctccaaa ctctacccga ctcatgcttg ccgggagtac ctgaaaaacc 720
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<211> 842
<212> DNA
<213> Artificial Sequence

<220>
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ggctatcggg aagacaacat cccgcaactg gaggatgtct ccaacttttt aaaagaacgc 180
actgggtttt ccatccgtcc tgtggctggt tacctctcac cgagagattt tctgtcgggg 240
ttagcctttc gagtctttca ctgcactcag tatgtgagac acagttcaga tcccctctac 300
actccagagc cagacacctg ccatgaactc ctaggccacg ttcctctctt ggctgaaccc 360
agttttgctc aattctccca agaaattggc ctggcttccc ttggagcttc agaggagaca 420
gttcaaaaac tggcaacgtg ctacttttc actgtggagt ttgggctgtg caaacaagat 480
ggacagctga gagtctttgg ggccggcttg ctttcttcca tcagtgaact caaacatgca 540
ctttctggac atgccaaagt caagcccttt gatcccaaga ttgcctgtaa acaggaatgt 600

ctcatcacga gcttccagga tgtctacttt gtatctgaga gctttgaaga tgcaaaggag 660
aagatgagag aatttgccaa gaccgtgaag cgcccgtttg gactgaagta caacccgtac 720
acacagagtg ttcaggttct cagagacacc aagagcataa ctagtgccat gaatgagttg 780
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<210> 8
<211> 21
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<223> Murine TPH2 forward primer mTPH2-1270F

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<210> 9
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<223> Murine TPH2 reverse primer mTPH2-585R

<400> 9
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<210> 10
<211> 21
<212> DNA
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<210> 11
<211> 27
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<400> 11
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<210> 12
<211> 26
<212> DNA
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<220>
<223> Murine TPH2 probe mTPH2-1292T

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